

8
DNT
3-20-02 1647



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/647,067

DATE: 02/13/2002

TIME: 12:54:10

Input Set : A:\SEQUENCE LISTIN1.txt

Output Set: N:\CRF3\02132002\I647067.raw

P.S.

RECEIVED

MAR 14 2002

TECH CENTER 1600/2900

ENTERED

4 <110> APPLICANT: Hsueh, Aaron J. W.
5 Hsu, Sheau Yu
6 Liang, Shan-Guang
7 Van Der Spek, Petrus Johannes
9 <120> TITLE OF INVENTION: Novel Mammalian G-Protein Coupled
10 Receptors Having Extracellular Leucine Rich Repeat Regions
13 <130> FILE REFERENCE: STAN-084
15 <140> CURRENT APPLICATION NUMBER: 09/647,067
16 <141> CURRENT FILING DATE: 2000-09-25
18 <150> PRIOR APPLICATION NUMBER: PCT/US99/06573
19 <151> PRIOR FILING DATE: 1999-03-25
21 <150> PRIOR APPLICATION NUMBER: 60/079,501
22 <151> PRIOR FILING DATE: 1998-03-26
24 <160> NUMBER OF SEQ ID NOS: 8
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 2856
30 <212> TYPE: DNA
31 <213> ORGANISM: homo sapiens
33 <400> SEQUENCE: 1
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35 cccagcggcg cggcgccggcc tctctgcgcg gcccgtca gctgcacgg cgaccgtcg 120
36 gtggactgtc ccggaaaggg gttgacggcc gtacggagg gtctcagcgc cttcacccaa 180
37 gcactggata tcagtatgaa caatatcacc cagttaccag aagatgcatt taagagttc 240
38 ccatttctag aggagctaca actggctggt aacgaccttt ctcttatcca tccaaaagcc 300
39 ttgtctgggc tgaaaagaact caaagtcccta acactccaga ataatcagg gagaacagt 360
40 cccagtgaag ccattcacgg actgagtgct ttgcagtctt tacgcttaga tgccaaaccat 420
41 attacctcag tccggagga cagtttggaa gggctgtcc agttacgcca tctgtggctg 480
42 gatgacaaca gcttgcggaa atgtccccgt cgtccctca gcaacctgcc aaccctgcag 540
43 gcgctgacct tggctctcaa caacatctca agcatccctg acttcgctt caccaacctt 600
44 tcaagcttgg tggttctgca tctgcataac aataaaattha aaagccttag tcaacactgt 660
45 tttgatggac tagataaccc gggaaaccttgc gacttgcatt acaatttactt ggatgagttt 720
46 cctcaggcta ttaaaggccct tcccaggcctt aaagagctgg gatttcacag taatttctatt 780
47 tctgttattc ctgatggagc atttgggtggt aatccactgc taagaactat tcatttgtat 840
48 gataatcctc tgtctttgtt gggaaactca gcatttcaca acctgtctga tctgcattgc 900
49 ttagtcattc gtgggtcaag cctgggtcag tggttccca atctgaccgg aactgtccat 960
50 ttggagagtc taaccttgac agggacaaaa ataagcagca tacctgtatca tctgtccaa 1020
51 aaccaaaaaga tgctgaggac tctggactta tcttataaca atataagaga ctttccaagt 1080
52 tttaatggtt gtcgtgcatt ggaagaaaatt tcattgcagc gtaatcaa atccctaata 1140
53 aaggaaaaata ctttcaagg cctaacatct ctaaggattc tagatctgag tagaaacctg 1200
54 atccgtgaaa ttcacagtgg agctttgcg aagctggga caattactaa cctggatgta 1260
55 agttcaatg aattaacttc atttcctacg gaaggctaa atgggctcaa tcaactaaag 1320
56 cttgtgggtt acttcaagct gaaagacgcc ttggcagcca gagactttgc taatctcagg 1380

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57 tctctatcag taccatatgc ttatcagtgt tgtgcatttt gggggtgtga ctcttatgc 1440
 58 aaattaaaca cagaagataa cagcccccaa gaacacagtg tgacaaaaga gaaaggtgct 1500
 59 acagatgcag caaatgtcac cagcaactgct gagaacgaag aacatagcca aataattatc 1560
 60 cactgtacac cttcaacagg tgccttcaag ccctgtgaat atttactggg aagctggatg 1620
 61 attcgccta cagtgtggtt cattttcctg gtcgccttgc ttttcaacct gcttgcatt 1680
 62 ttaacagtgt ttgcgtctt ttcataactg cctgcctcca aactcttcat aggcttgatt 1740
 63 tctgtgtcta acttactcat gggcatctat actggcatcc ttactttct ttagtgcgtg 1800
 64 tcctggggcc gatttgcga atttggcatt tggggaaa ctggcagcgg ctgcaaggta 1860
 65 gccgggtctc tggcagtctt ctccctcagag agcgctgtat tcctattaac actggcagct 1920
 66 gtggaaagaa gcgtatttgc aaaggatttg atgaaacacg ggaagagcag tcacccaga 1980
 67 cagttccagg tggcccccct ctagcttt ctgggtgccg cagttggcagg ctgcttcccc 2040
 68 cttttccacg gagggaata ttctgcacacg cccttgcgtt tgccgtttcc tacaggagaa 2100
 69 accccatcgt taggattcac tgcgtaccca gtgctattaa actcaactgatc attttacta 2160
 70 atggccatta tctacactaa actataactgc aacttagaga aggaggacat gtcgaaaaac 2220
 71 tcccaagtcta gcgtgattaa gcacgttgc tggctcatct tcacaaactg catcttctc 2280
 72 tgccctgttg cattttctc atttgcacca ttgatcacgg caatctccat cagccccgag 2340
 73 ataatgaagt ctgttacact gatattcttcc cggttgcctg cttgcctgaa tccgtcctg 2400
 74 tatgtttct tcaacccaaa gttaaagaa gactgaagc tactgaagc gcgtgttacc 2460
 75 agggaaacacg gatcttttc agtttccatc agcagccaag gcgggtgtgg ggaacaggat 2520
 76 ttctactatg actgtggcat gtattccac ttgcagggtt acctgactgt ctgtgactgc 2580
 77 tgtgagtcat ttctttgac aaaaccagta tcatgcaaac acttaataaa atcgcacagt 2640
 78 tgtcctgtat tgacagcggc ctcttgccag aggccagagg cctactggc tgattgttgt 2700
 79 acacagttag cccattctga ctatgcagat gaagaagatt ctttgcctc agacagctct 2760
 80 gaccagggtgc aggccctgtgg acgagcctgc ttctaccaga gtcgtggatt ccctctgggt 2820
 81 cgctatgctt acaatctaca gagagtca gactga 2856

83 <210> SEQ ID NO: 2

84 <211> LENGTH: 951

85 <212> TYPE: PRT

86 <213> ORGANISM: human

88 <400> SEQUENCE: 2

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90	1				5			10				15				
91	Gly	Ser	Ala	Gly	Pro	Ser	Gly	Ala	Ala	Pro	Pro	Ley	Cys	Ala	Ala	Pro
92					20			25				30				
93	Cys	Ser	Cys	Asp	Gly	Asp	Arg	Arg	Val	Asp	Cys	Ser	Gly	Lys	Gly	Ley
94					35			40			45					
95	Thr	Ala	Val	Pro	Glu	Gly	Ley	Ser	Ala	Phe	Thr	Gln	Ala	Ley	Asp	Ile
96					50			55			60					
97	Ser	Met	Asn	Asn	Ile	Thr	Gln	Ley	Pro	Glu	Asp	Ala	Phe	Lys	Ser	Phe
98	65					70			75			80				
99	Pro	Phe	Ley	Glu	Glu	Ley	Gln	Ley	Ala	Gly	Asn	Asp	Ley	Ser	Ley	Ile
100					85			90			95					
101	His	Pro	Lys	Ala	Ley	Ser	Gly	Ley	Lys	Glu	Ley	Lys	Val	Ley	Thr	Ley
102					100			105			110					
103	Gln	Asn	Asn	Gln	Ley	Arg	Thr	Val	Pro	Ser	Glu	Ala	Ile	His	Gly	Ley
104					115			120			125					
105	Ser	Ala	Ley	Gln	Ser	Ley	Arg	Ley	Asp	Ala	Asn	His	Ile	Thr	Ser	Val
106					130			135			140					
107	Pro	Glu	Asp	Ser	Phe	Glu	Gly	Ley	Val	Gln	Ley	Arg	His	Ley	Trp	Ley

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108	145	150	155	160
109	Asp Asp Asn Ser Leu Thr Glu Val Pro Val Arg Pro Leu Ser Asn Leu			
110	165.	170	175	
111	Pro Thr Leu Gln Ala Leu Thr Leu Ala Leu Asn Asn Ile Ser Ser Ile			
112	180	185	190	
113	Pro Asp Phe Ala Phe Thr Asn Leu Ser Ser Leu Val Val Leu His Leu			
114	195	200	205	
115	His Asn Asn Lys Ile Lys Ser Leu Ser Gln His Cys Phe Asp Gly Leu			
116	210	215	220	
117	Asp Asn Leu Glu Thr Leu Asp Leu Asn Tyr Asn Tyr Leu Asp Glu Phe			
118	225	230	235	240
119	Pro Gln Ala Ile Lys Ala Leu Pro Ser Leu Lys Glu Leu Gly Phe His			
120	245	250	255	
121	Ser Asn Ser Ile Ser Val Ile Pro Asp Gly Ala Phe Gly Gly Asn Pro			
122	260	265	270	
123	Leu Leu Arg Thr Ile His Leu Tyr Asp Asn Pro Leu Ser Phe Val Gly			
124	275	280	285	
125	Asn Ser Ala Phe His Asn Leu Ser Asp Leu His Cys Leu Val Ile Arg			
126	290	295	300	
127	Gly Ala Ser Leu Val Gln Trp Phe Pro Asn Leu Thr Gly Thr Val His			
128	305	310	315	320
129	Leu Glu Ser Leu Thr Leu Thr Gly Thr Lys Ile Ser Ser Ile Pro Asp			
130	325	330	335	
131	Asp Leu Cys Gln Asn Gln Lys Met Leu Arg Thr Leu Asp Leu Ser Tyr			
132	340	345	350	
133	Asn Asn Ile Arg Asp Leu Pro Ser Phe Asn Gly Cys Arg Ala Leu Glu			
134	355	360	365	
135	Glu Ile Ser Leu Gln Arg Asn Gln Ile Ser Leu Ile Lys Glu Asn Thr			
136	370	375	380	
137	Phe Gln Gly Leu Thr Ser Leu Arg Ile Leu Asp Leu Ser Arg Asn Leu			
138	385	390	395	400
139	Ile Arg Glu Ile His Ser Gly Ala Phe Ala Lys Leu Gly Thr Ile Thr			
140	405	410	415	
141	Asn Leu Asp Val Ser Phe Asn Glu Leu Thr Ser Phe Pro Thr Glu Gly			
142	420	425	430	
143	Leu Asn Gly Leu Asn Gln Leu Lys Leu Val Gly Asn Phe Lys Leu Lys			
144	435	440	445	
145	Asp Ala Leu Ala Ala Arg Asp Phe Ala Asn Leu Arg Ser Leu Ser Val			
146	450	455	460	
147	Pro Tyr Ala Tyr Gln Cys Cys Ala Phe Trp Gly Cys Asp Ser Leu Cys			
148	465	470	475	480
149	Lys Leu Asn Thr Glu Asp Asn Ser Pro Gln Glu His Ser Val Thr Lys			
150	485	490	495	
151	Glu Lys Gly Ala Thr Asp Ala Ala Asn Val Thr Ser Thr Ala Glu Asn			
152	500	505	510	
153	Glu Glu His Ser Gln Ile Ile Ile His Cys Thr Pro Ser Thr Gly Ala			
154	515	520	525	
155	Phe Lys Pro Cys Glu Tyr Leu Leu Gly Ser Trp Met Ile Arg Leu Thr			
156	530	535	540	

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157 Val Trp Phe Ile Phe Leu Val Ala Leu Leu Phe Asn Leu Leu Val Ile
158 545 550 555 560
159 Leu Thr Val Phe Ala Ser Cys Ser Ser Leu Pro Ala Ser Lys Leu Phe
160 565 570 575
161 Ile Gly Leu Ile Ser Val Ser Asn Leu Leu Met Gly Ile Tyr Thr Gly
162 580 585 590
163 Ile Leu Thr Phe Leu Asp Ala Val Ser Trp Gly Arg Phe Ala Glu Phe
164 595 600 605
165 Gly Ile Trp Trp Glu Thr Gly Ser Gly Cys Lys Val Ala Gly Ser Leu
166 610 615 620
167 Ala Val Phe Ser Ser Glu Ser Ala Val Phe Leu Leu Thr Leu Ala Ala
168 625 630 635 640
169 Val Glu Arg Ser Val Phe Ala Lys Asp Leu Met Lys His Gly Lys Ser
170 645 650 655
171 Ser His Leu Arg Gln Phe Gln Val Ala Ala Leu Leu Ala Leu Leu Gly
172 660 665 670
173 Ala Ala Val Ala Gly Cys Phe Pro Leu Phe His Gly Gly Gln Tyr Ser
174 675 680 685
175 Ala Ser Pro Leu Cys Leu Pro Phe Pro Thr Gly Glu Thr Pro Ser Leu
176 690 695 700
177 Gly Phe Thr Val Thr Leu Val Leu Leu Asn Ser Leu Ala Phe Leu Leu
178 705 710 715 720
179 Met Ala Ile Ile Tyr Thr Lys Leu Tyr Cys Asn Leu Glu Lys Glu Asp
180 725 730 735
181 Leu Ser Glu Asn Ser Gln Ser Ser Val Ile Lys His Val Ala Trp Leu
182 740 745 750
183 Ile Phe Thr Asn Cys Ile Phe Phe Cys Pro Val Ala Phe Phe Ser Phe
184 755 760 765
185 Ala Pro Leu Ile Thr Ala Ile Ser Ile Ser Pro Glu Ile Met Lys Ser
186 770 775 780
187 Val Thr Leu Ile Phe Phe Pro Leu Pro Ala Cys Leu Asn Pro Val Leu
188 785 790 795 800
189 Tyr Val Phe Phe Asn Pro Lys Phe Lys Glu Asp Trp Lys Leu Leu Lys
190 805 810 815
191 Arg Arg Val Thr Arg Lys His Gly Ser Val Ser Val Ser Ile Ser Ser
192 820 825 830
193 Gln Gly Gly Cys Gly Glu Gln Asp Phe Tyr Tyr Asp Cys Gly Met Tyr
194 835 840 845
195 Ser His Leu Gln Gly Asn Leu Thr Val Cys Asp Cys Cys Glu Ser Phe
196 850 855 860
197 Leu Leu Thr Lys Pro Val Ser Cys Lys His Leu Ile Lys Ser His Ser
198 865 870 875 880
199 Cys Pro Val Leu Thr Ala Ala Ser Cys Gln Arg Pro Glu Ala Tyr Trp
200 885 890 895
201 Ser Asp Cys Gly Thr Gln Ser Ala His Ser Asp Tyr Ala Asp Glu Glu
202 900 905 910
203 Asp Ser Phe Val Ser Asp Ser Ser Asp Gln Val Gln Ala Cys Gly Arg
204 915 920 925
205 Ala Cys Phe Tyr Gln Ser Arg Gly Phe Pro Leu Val Arg Tyr Ala Tyr

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206	930	935	940							
207	Asn	Leu	Gln	Arg	Val	Arg	Asp			
208	945			950						
211	<210>	SEQ ID NO:	3							
212	<211>	LENGTH:	2082							
213	<212>	TYPE:	DNA							
214	<213>	ORGANISM:	homo sapiens							
216	<220>	FEATURE:								
217	<221>	NAME/KEY:	misc_feature							
218	<222>	LOCATION:	768							
219	<223>	OTHER INFORMATION:	n = A,T,C or G							
221	<400>	SEQUENCE:	3							
222	ctacatctcc	ataacaatag	aatccactcc	ctggaaaga	aatgc	tttga	tggctccac	60		
223	agcctagaga	ctttagattt	aaattacaat	aac	ctt	gatg	aattcccac	tgcaattagg	120	
224	acactctcca	acttaaagga	actaggattt	catagcaaca	atatc	caggtc	gatac	ctgag	180	
225	aaagcatttg	taggcaaccc	ttctcttatt	acaatacatt	tctat	gaccaa	tcc	catccaa	240	
226	tttgttggga	gatctgttt	tcaacattt	cctgaactaa	gaacactgac	tctgaatgg	gt	atgg	300	
227	gcctcacaaa	taactgaatt	tcctgattt	actgaaactg	caaacc	tgg	gagt	ctgact	360	
228	ttaactggag	cacagatctc	atctcttct	caaaccgtct	gcaat	cagtt	accta	atctc	420	
229	caagtgttag	atctgttta	caaccttatt	gaagatttac	ccagttt	tc	agt	ctgcca	480	
230	aagcttcaga	aaatttgcac	aagacataat	gaaatctacg	aaatta	aaagt	tgac	actttc	540	
231	cagcagttgc	ttagcctccg	atcgctgaat	ttggcttgg	aca	aaaat	tg	tatttac	600	
232	cccaatgcat	tttccacttt	gccatcccta	ataaaagctgg	ac	ctat	cg	caac	ctctg	660
233	tcgtctttc	ctataactgg	gttacatgt	ttaactcact	taaaat	taa	agg	aaat	cat	720
234	gccttacaga	gctggatatc	atctgaaaac	tttccagaac	tcaaggtnat	agaaatgcct				780
235	tatgc	tacc	agtgc	tgtgc	at	tttgg	agtg	tgt	gagaat	840
236	tgaat	aaag	gtgac	aaacag	cag	tat	ggac	gac	tgg	900
237	cagg	ctcaag	atg	aacgt	gt	c	tgg	atgtt	gag	960
238	gcc	tttcatt	cag	tgc	act	ttc	acc	cc	tgc	1020
239	ctt	gtatgg	gt	gc	at	tttgg	gag	tgg	accat	1080
240	aat	gctt	gg	ct	ac	tttgc	at	tgc	tgt	1140
241	tta	atttgg	gg	tca	tgc	at	tttgc	at	tttgc	1200
242	gg	tgttgg	at	gtt	act	tttgc	tttgc	at	tttgc	1260
243	gtt	gggttgc	at	gt	catttgc	tttgc	at	tttgc	tttgc	1320
244	ctt	act	cttgc	tttgc	at	tttgc	at	tttgc	tttgc	1380
245	aa	agctccat	tttct	at	tttgc	at	tttgc	at	tttgc	1440
246	at	ggccgc	at	tttgc	at	tttgc	at	tttgc	tttgc	1500
247	tttgc	tttttgc	at	tttgc	at	tttgc	at	tttgc	tttgc	1560
248	tttgc	tttgc	at	tttgc	at	tttgc	at	tttgc	tttgc	1620
249	gac	cttgc	at	tttgc	at	tttgc	at	tttgc	tttgc	1680
250	aa	actgc	at	tttgc	at	tttgc	at	tttgc	tttgc	1740
251	ttt	atc	at	tttgc	at	tttgc	at	tttgc	tttgc	1800
252	ctca	atcccc	tttgc	at	tttgc	at	tttgc	at	tttgc	1860
253	agaa	agc	aa	cctac	gtc	at	ttgc	at	tttgc	1920
254	gat	gtatgt	tc	aaaaac	atgc	at	ttgc	at	tttgc	1980
255	agc	atc	at	tttgc	at	tttgc	at	tttgc	tttgc	2040
256	actgc	atc	tttgc	at	tttgc	at	tttgc	at	tttgc	2082
258	<210>	SEQ ID NO:	4							
259	<211>	LENGTH:	693							

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/647,067

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Input Set : A:\SEQUENCE LISTIN1.txt

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L:234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7